SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Bergmann, Johanna & Preddie, Rick
- (ii) TITLE OF INVENTION: AGENTS FOR PRESYMPTOMATIC DIAGNOSIS AND THERAPEUTIC TARGETING IN HUMAN ALZHEIMER'S DISEASE AND DOWN SYNDROME

BO BOND TO THE CONTROL PRODUCT OF THE CONTROL CONT

(iii) NUMBER OF SEQUENCES:

- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: DR. J. BERGMANN
 - (B) STREET: MÖRIKESTR. 22
- (C) CITY: HAMBURG
- Barka (1980-black)(D) STATE: proceed with the later and India for a real from the content of the real end by the first black for
 - (E) COUNTRY: GERMANY

 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #125
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: NONE
 - (B) REGISTRATION NUMBER:
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (4940) 86662948
 - (B) TELEFAX: (4940) 86662949 or (4940) 862596

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 240 base pairs
 - (B) TYPE: nucleic acid
 - (D) TOPOLOGY: linear
 - (C) STRANDNESS: single
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: alzas
- (xi) SEQUENCE DESCRIPTION: SEQ-ID NO.1:

ATGGATGCAG AATTCCGACA TGACTCAGGA TATGAAGTTC ATCATCAAA 50
AATTGGTGTT CTTTGCAGAA GATGTGGGTT CAAACAAAGG TGCAATCATT 100
GGACTCATGG TGGGCGGTGT TGTCATAGCG ACAGTGATCG TCATCACCTT 150
GGTGATGCTG AAGAAGAAAC AGTACACATC CATTCATCAT GGTGTGGTGG 200
AGGTAGGTAA ACTTGACTGC ATGTTTCCAA GTGGGAATTA A 240

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- (2) INFORMATION FOR SEQ ID NO:2:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 79 amino acids
 - (B) TYPE: amino acid.
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (vii) IMMEDIATE SOURCE:
 - (B) CLONE: ALZASp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2

Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His
5 10 15

Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly 20 25 30

Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val 35 40 45

Ile Val Ile Thr Leu Val Met Leu Lys Lys Gln Tyr Thr Ser 50 55 60

Ile His HIs Gly Val Val Glu Val Gly Lys Leu Asp Cys Met Phe
65 70 75

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Pro Ser Gly Asn

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 amino acids
- un alterno more (B). TYPE: amino acid no come service actes in the come and make the come at the come at the come
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL: yes
 - (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

- (vii) IMMEDIATE SOURCE:_
 - (B) CLONE: ALZASp
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Gln Asn Ser Asp Met Thr Gln Asp Met Lys Phe Ile Ile Lys
5 10 15

Asp Trp Cys Ser Leu Glu Lys Met Trp Val Gln Thr Lys Val Gln 20 25 30

Ser Leu Asp Ser Trp Trp Ala Val Leu Ser

35 40

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: Yes
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: ALZASp
- The state of the sequence description: SEQ ID NO.4. Historian control of the sequence of the s

الأصافرة اليجوان المعاصر فيداعف مخصد والدراء ومعوالفسف بياسي أجازات المارا المرافر الروحان أأخطأ فركرة المسارخيات Met Gln Asn Ser Asp Met Thr Gln Asp Met Lys Phe Ile Ile Lys

elakurun madirim keput terdapun 14. di tegu 17. dik dimekan terdapun pengengan di mekan keput melajak menjuli

Asn Trp Tyr Val Lys

20

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 156 base pairs
 - (B) TYPE: nucleic acid
 - (D) TOPOLOGY: linear
 - (C) STRANDNESS: single
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (vii) IMMEDIATE SOURCE:

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(B) CLONE:alzas1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGGATGCAG AATTCCGACA TGACTCAGGA TATGAAGTTC ATCATCAAAA 50 ATTGGTACGT AAAATAATTT ACCTCTTTCC ACTACTGTTT GTCTTGCCAA 100 ATGACCTATT AACTCTGGTT CATCCTGTGC TAGAAATCAA ATTAAGGAAA 150 AGATAA 156

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- (2) INFORMATION FOR SEQ ID NO:6:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

(B) CLONE: ALZAS1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Asp Ala GLu Phe Arg His Asp Ser Gly Tyr Glu Val His His 5 10 15

Gln Lys Leu Val Arg Lys Ile Ile Tyr Leu Phe Pro Leu Leu Phe 20 25 30

Val Leu Pro Asn Asp Leu Leu Thr Leu Val His Pro Val Leu Glu
35 40 45

Ile Lys Leu Arg Lys Arg 50

- (2) INFORMATION FOR SEQ ID NO:7:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 79 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: PALZ1
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTGATAATTA AATGTTATAG CATGGACACT GACATTTACA TTTTTTACTT 50 ATGTTTTTGG TTTTTAAATG ACTCTGCAT 79

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- (2) INFORMATION FOR SEQ ID NO:8:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Genomic DNA
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (vii) IMMEDIATE SOURCE:
 - (B) CLONE: PALZ2
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATTATTATTT GAATAATGAA ATTCATCAGA ACAATTA 37

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 base pairs
 - (B) TYPE: nucleic acid
 - (D) TOPOLOGY: linear
 - (C) STRANDNESS: single
- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE:PALZ3
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCAATTTATA GAAAAGGAAG AGTTCGTAGG TTATAAATTC TGTTAGTTGC 60 TAAGAAGCAT TTTTAAAA 68

- (2) INFORMATION FOR SEQ ID NO:10:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (D) TOPOLOGY: linear
 - (C) STRANDNESS: single
 - (ii) MOLECULE_TYPE: genomic DNA
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (vii) IMMEDIATE SOURCE:
 - (B) CLONE:PALZ4

38

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATGCTCATTT TTAAAGGCTT TTATTATTAT TTCTGAAGTA ATGAGTGCAC 50 ATGGAAAAA 59

- (2) INFORMATION FOR SEQ ID NO:11:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (D) TOPOLOGY: linear
 - (C) STRANDNESS: single
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (vii) IMMEDIATE SOURCE:
 - (B) CLONE:PALZ5
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TATTCCAGGA ACAAATCCTT GCCAACCTCT CAACCAGG

- (2) INFORMATION FOR SEQ ID NO:12:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (D) TOPOLOGY: linear
 - (C) STRANDNESS: single
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

- (vii) IMMEDIATE SOURCE: (B) CLONE:PALZ6
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TAGCATGTAT TTAAATGCAG CAGAAG 26

- (2) INFORMATION FOR SEQ ID NO:13:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (D) TOPOLOGY: linear
 - (C) STRANDNESS: single
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (vii) IMMEDIATE SOURCE:
 - (B) CLONE:PALZ7
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAAGGTTTAA ATATAGGGTA TCATTTTCT TTAAGAGTCA TTTATCAATT 50 TTCTTC 56

- (2) INFORMATION FOR SEQ-ID-NO:14:----
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 170 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO

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- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE:alzas2
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATGTGGGTTC AAACAAAGGT GCAATCATTG GACTCATGGT GGGCGGTGTT 50 GTCATAGCGA CAGTGATCGT CATCACCTTG GTGATGCTGA AGAAGAAACA 100 GTACACATCC ATTCATCATG GTGTGGTGGA GGTAGGTAAA CTTGACTGCA 150 TGTTTCCAAG TGGGAATTAA 170

- (2) INFORMATION FOR SEQ ID NO:15:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (vii) IMMEDIATE SOURCE:
 - (B) CLONE: ALZAS4
 - (xi) SEQUENCE DESCRIPTION SEQ ID NO:15:

Met Val Gly GLy Val Val Ile Ala Thr Val Ile Val Ile Thr Leu
5 10 15

Val Met Leu Lys Lys Gln Tyr Thr Ser Ile His His Gly Val

20 25 30

Val Glu Val Gly Lys Leu Asp Ser Trp Trp Ala Val Leu Ser 35 40

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (vii) IMMEDIATE SOURCE:

(B) CLONE: ALZAS5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

10

Met Val Trp Gln Thr Lys Val Gln Ser Leu Asp Ser Trp Trp Ala

ng kalangan saken tidak di kalangan beraga pengangganggan panggan kalangan di kanggan di keragan di keragan di

Val Leu Ser

- (2) INFORMATION FOR SEQ ID NO:17:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: YES
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (vii) IMMEDIATE SOURCE:
 - (B) CLONE:PALZ9
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (vii) IMMEDIATE SOURCE: CLONE: PALZ10
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

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TTATGCTTTA AAAAGCAATA CA

22

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: HOMO SAPIENS
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: PALZ11
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CTTTTTATAT AACCTCATCC AAATGTCCCC TGCATTTAA

39

- (2) INFORMATION FOR SEQ ID NO:22:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: HOMO SAPIENS
 - (vii) IMMEDIATE SOURCE:
 - (B) CLONE: PALZ14
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GAAAATGAAA TTCTTCTAAT TGCGTTTATA AATTGTAATT A 41